



Sequence Listing

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagcttctg gtgccttttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataacct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
ggcccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350
tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
gaggatcttc tccttcttcc cagttccagt cacagtgagg gcgcattctca 500
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tatcctgggt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150
gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200
tggantttgc ctttgcagaa ntttgnngtg ttcctttgcg gattttctcc 250
tttttcccag ttccagtcac agngaggggc catctcaccg ggnggntgat 300

gacantgaag aaaacotttg tcoctgcccc cagctntttg gtgoggatca 350
ttgtctnat ngccagcctt gtggctctac ctacctggg ggtgcacggt 400
ggacccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccaagt tccggtcacg gggagggcgc atntcacagg gtggctgang 50
aacctgaaga aaaccttngt ccttgccccc agntttgtgn tgcggatnat 100
cgctctcacc gccagcctng tggctctacc ctacctggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcctctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gactgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50
gctgcttg gagcctgtc cctgtcagc tgcgcgtcct gctctgcgg 100
ctctgcccc tgcatcctgt gcagctgtg ccccgccagc cgcaactcca 150

cogtgagcog cctcatcttc acgttcttcc tcttctggg ggtgctggtg 200
tccatcatta tgetgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtctgt cagggccaca 300
tcgactgtgg ctccctgctt ggctaccggt ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttt accctgctca tgctctgcgt 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctgggt ggctcaccg tgggtgcctt ctacatccct 500
gacggctcct tcaccaacat ctgggtctac ttccggcgtcg tgggtcctt 550
cctcttcctc ctcatccagc tgggtgctgt catcgacttt ggcactcct 600
ggaaccagcg gtggtggggc aaggccgagg agtgcgattc cegtgcctgg 650
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700
ggcgtggcg ctgatgttca tglactacac tgagcccagc ggtgccacg 750
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gctgcaggcc tcggtcatca cctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950
ctgggcaacg agacagtgtt ggcaggcccc gagggctatg agaccagtg 1000
gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050
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cagaccgagg agtgcctacc tatgctagac gccacacagc agcagcagca 1150
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
tcacctacag ctactccttc ttccacttct gcctggtgct ggctcactg 1250
cacgtcatga tgacgtcac caactggtac aagcccgtg agaccggaa 1300
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
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aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctc 1450
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
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caggctctctg cagagcccca tccccccgccc acaccacacac ggtggagctg 1650
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ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
tggtcacgtc cccagggga cctgcccc ttcttgact tegtgcctta 1850
ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	1	5	10	15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	20	25	30	
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	35	40	45	
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly	50	55	60	
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75	
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90	
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105	
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120	
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135	
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150	
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165	
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180	

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcattccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttccac ttctgcctgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc acgg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcaccac acg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtcatcat tatgctgagc ccggcggtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctcgtaacagt tacgtctctc 100
cgcggcacgt ccgcgaggac ttgaagtccct gagcgctcaa gtttgtccgt 150
aggctcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250
actgccgatt cggaagtccct tgaggagcgt cagaagcggc ttcctacgt 300
cccagagccc tattaccgg aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgag gagctgtcac ggggaagtctt 700
tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750
agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctgggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
 atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000
 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050
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 gtactctcac tttacttata ctttaaattta aatacatact tatgtttgta 1250
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
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 t 1351

<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala	1	5	10	15
Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala	20	25	30	
Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45	
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60	
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75	
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90	
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105	
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120	
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135	

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

cggaagtccc ttgaggagcg tcagaagcgg ctccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

cgggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

tctgttcattg gctggcgccg aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
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accgcggagc tttttctgt agagcattgt gctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcgga gtccttgagg agcgtcagaa 150
ggcgcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
tttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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ccacccacgt ctgcgttgct gcccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgcgc gagtcgaatt tacgtgcagc 150
tgcgcgcaac cacaggttcc aagatgggtt gggggggctt cgcgtgttcc 200
aagaactgcc tgtgcgcctt caacctgctt tacaccttg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300
tccgagtggc cggcgtggtc attgcagtgg gcattctctt gttcctgatt 350
gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttcttatt 400
tttttatatg attattctgt tacttgattt tattgttcag ttttctgtat 450
cttgcgcttg tttagccctg aaccaggagc aacagggcca gcttctggag 500
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550
aaactgctgt gggttccgaa gtgttaaccc aaatgacacc tgtctggcta 600
gctgtgttaa aagtgaccac tcgtgtcgc catgtgtcc aatcatagga 650
gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700
cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800
gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850
taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
ctattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950
ttttctttcc gttgctgaaa aatatttgaa acttgtggtc tctgaagctc 1000
ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
cctttcttag catttttacc tgcagaaaaa ctttgatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactggtat aatttatatgt 1150
 agcaactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaaatcaga aagtatgaga tccgtgttatg ttaagggaaa tccaaattcc 1250
 caatTTTTTT ttggtctTTTT aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acattttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattggtt tataataatt tgaagtctaa 1550
 aagactgcat ttttaaaca gttagtatta atgcgttggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
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 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
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 35 40 45
 Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
 50 55 60
 Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
 65 70 75
 Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
 80 85 90
 Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly
 95 100 105

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn
110 115 120

Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn
125 130 135

Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser
140 145 150

Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val
155 160 165

Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu
170 175 180

Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp
185 190 195

Pro Arg Ala Asn Pro Ser Ala Phe Leu
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<210> 37

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336

<223> unknown base

<400> 37

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tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttgtt 100

tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tgggtggaac 150

aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200

gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250

gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350

gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttggnctt tttagggaaa gatgtgttgt 50
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tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgag 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgtttagc cctgaaacc aggagcaaca gggnnccagct tcctggaggt 100
tggttggaac caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200
tggtctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
 aacacagctct gcggttgcctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
 gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
 aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
 ggcccaaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
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 gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
 cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200
 tacactttca gtgaacctt ccacctgatt gtgtcctatg actggtgat 250
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<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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Leu	Gly	Val	Leu	Trp	Val	Ala	Gln	Met	Leu	Leu	Ala	Ala	Ser	Phe	20	25	30	
Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	35	40	45	
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	50	55	60	
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val	65	70	75	
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe	80	85	90	
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp	95	100	105	
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly	110	115	120	
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys	125	130	135	
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro	140	145	150	
Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195	

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	
				200					205					210	
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	
				215					220					225	
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	
				230					235					240	
Glu	Ala	Ala	Thr	Ile	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	
				245					250					255	
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	
				260					265					270	
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	
				275					280					285	
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	
				290					295					300	
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	
				305					310					315	
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	
				320					325					330	
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	
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<210> 46
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 tgggctgtgt cctcatgg 18

<210> 47
 <211> 18
 <212> DNA
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<220>
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<400> 47
 tttccagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

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<210> 52

<211> 321

<212> PRT

<213> Homo sapiens

<400> 52

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Asp	Thr	Tyr	Gly	Arg	Pro	Ile	Leu	Glu	Val	Pro	Glu	Ser	Val	Thr
				20					25					30
Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro
				35					40					45
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg
				50					55					60
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp
				65					70					75
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His
				80					85					90
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met
				95					100					105
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro
				110					115					120
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val
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Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly
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Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys
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Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln
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Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr
				185					190					195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	
				200					205					210	
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	
				215					220					225	
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
				230					235					240	
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
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Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	
				260					265					270	
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	
				275					280					285	
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	
				290					295					300	
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	
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<210> 53
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<220>
 <223> Synthetic oligonucleotide probe

<400> 53
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<210> 54
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 <212> DNA
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 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
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<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

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<210> 59
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 59
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 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
 140 145 150
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

170	175	180
Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu	
185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

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<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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				20					25					30	
Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	
				35					40					45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
				110					115					120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
				260					265					270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
				275					280					285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val
575 580 585

Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe
590 595 600

Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile
605 610 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
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Ser Val Tyr Ser His Leu Pro Asp Leu Leu
650 655

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

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<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctctgtgtt ggattcctta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35				40						45

Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50						55						60
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly		
				65					70					75		
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala		
				80					85					90		
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr		
				95					100					105		
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe		
				110					115					120		
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly		
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His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr		
				140					145					150		
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe		
				155					160					165		
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys		
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Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala		
				185					190					195		
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg		
				200					205					210		
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu		
				215					220					225		
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His		
				230					235					240		
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala		
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Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile		
				260					265					270		
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His		
				275					280					285		
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg		
				290					295					300		
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr		
				305					310					315		
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu		
				320					325					330		
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala		

335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala		
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr		
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr		
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val		
395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe		
410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg		
425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp		
440	445	450
Leu Lys Thr		

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 70
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<210> 71
 <211> 24
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 71
 tacacgtccc tgtggttgca gatc 24

<210> 72
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<220>
 <223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly
				20					25				30	
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala
				35					40				45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp
				50					55				60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu
				65					70				75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile
				80					85				90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp
				95					100				105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly
				110					115				120	

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctaccaggga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150
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agcaagggtt gggcccagtg tcccctttcc ccagtgcacac ctcagccttg 350
gcagccctga taactggtn ntggctgcaa nttaatgctn tgatatggct 400
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gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggc ctcagg 27

<210> 77

<211> 18

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<400> 77
catgagcatg tgcacggc 18

<210> 78
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
tacctgcacg atgggcac 18

<210> 79
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
caactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 81
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<210> 82
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
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gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
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 20 25 30
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
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<210> 87
<211> 29
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<220>
<223> Synthetic oligonucleotide probe

<400> 87
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<210> 88
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<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 89
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<212> DNA
<213> Homo sapiens

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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

Met	Pro	Ala	Arg	Pro	Gly	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Arg	Pro
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Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20					25				30	

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35					40				45	

Ala Asp Gly Pro	Pro Ala Ala Asp Gly	Glu Asp Gly Gln Asp	Pro
50		55	60
His Ser Lys His	Leu Tyr Thr Ala Asp Met	Phe Thr His Gly Ile	
65	70		75
Gln Ser Ala Ala	His Phe Val Met Phe	Phe Ala Pro Trp Cys Gly	
80	85		90
His Cys Gln Arg	Leu Gln Pro Thr Trp Asn	Asp Leu Gly Asp Lys	
95	100		105
Tyr Asn Ser Met	Glu Asp Ala Lys Val Tyr	Val Ala Lys Val Asp	
110	115		120
Cys Thr Ala His	Ser Asp Val Cys Ser	Ala Gln Gly Val Arg Gly	
125	130		135
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro	Gly Gln Glu Ala Val Lys	
140	145		150
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr	Leu Glu Asn Trp Met Leu	
155	160		165
Gln Thr Leu Asn	Glu Glu Pro Val Thr	Pro Glu Pro Glu Val Glu	
170	175		180
Pro Pro Ser Ala	Pro Glu Leu Lys Gln	Gly Leu Tyr Glu Leu Ser	
185	190		195
Ala Ser Asn Phe	Glu Leu His Val Ala	Gln Gly Asp His Phe Ile	
200	205		210
Lys Phe Phe Ala	Pro Trp Cys Gly His	Cys Lys Ala Leu Ala Pro	
215	220		225
Thr Trp Glu Gln	Leu Ala Leu Gly Leu	Glu His Ser Glu Thr Val	
230	235		240
Lys Ile Gly Lys	Val Asp Cys Thr Gln	His Tyr Glu Leu Cys Ser	
245	250		255
Gly Asn Gln Val	Arg Gly Tyr Pro Thr	Leu Leu Trp Phe Arg Asp	
260	265		270
Gly Lys Lys Val	Asp Gln Tyr Lys Gly	Lys Arg Asp Leu Glu Ser	
275	280		285
Leu Arg Glu Tyr	Val Glu Ser Gln Leu	Gln Arg Thr Glu Thr Gly	
290	295		300
Ala Thr Glu Thr	Val Thr Pro Ser Glu	Ala Pro Val Leu Ala Ala	
305	310		315
Glu Pro Glu Ala	Asp Lys Gly Thr Val	Leu Ala Leu Thr Glu Asn	
320	325		330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
425 430

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

atgttcttcg cgccctggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtggtcgc cttgtgcaac gtgc 24

<210> 94

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtc aaagg gatatacgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200
agaggggaaag catggcaaag tgggacgcat ggggcccgaag ggaattaaag 250
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attgggaaga agggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350
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 cagttattgt tatccatcct ttttttctg attgtactac atttgatctg 950
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 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
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 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200		205		210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn					
	215		220		225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser					
	230		235		240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly					
	245		250		255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys					
	260		265		270
Glu Phe Ile Lys Lys Lys Lys					
	275				

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
 cgctgactat gttgcccaaga gtgg 24

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 99
 gatgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 100
 gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 101
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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
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 catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys	320	325	330
Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala		335	340	345
Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln		350	355	360
Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro		365	370	375
Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met		380	385	390
Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly		395	400	405
Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln		410	415	420
Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser		425	430	435
Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly		440	445	450
Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro		455	460	465
Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala		470	475	480
Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser		485	490	495
Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp		500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met		515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser		530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala		545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe		560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu		575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu		590	595	600

Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp
				605					610					615
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His
				620					625					630
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His
				635					640					645
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu
				650					655					660
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu
				665					670					675
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn
				680					685					690
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu
				695					700					705
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr
				710					715					720
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile					
				725					730					

<210> 103
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 103
 gagagccatg gggctccacc tg 22

<210> 104
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<220>
 <223> Synthetic oligonucleotide probe

<400> 104
 ggagaatgtg gccacaac 18

<210> 105
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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acgcgcgcac acacactcgc tctcgtttgt ccatctccct cccgggggag 150
ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgc 200
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 attgtcctgg cactgcagag actgtgcaga taatcttggg tttttggtca 2250
 gatgaaactg cattttagct atctgaatgg ccaactcact tcttttctta 2300
 cactcttggg caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350
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 gggtgccaga ctgaactgct tctcttttcc ttcagctatc tgtggggacc 2450
 ttgtttatcc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550
 gtgagggttt tttttttctc atttaaaat 2579

<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
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 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75
 Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr
 80 85 90
 Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe
 95 100 105
 Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu
 110 115 120
 Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn
 125 130 135
 Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr
 140 145 150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp
440 445 450

Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met
455 460 465

Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly
470 475 480

Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser
485 490 495

Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe
500 505 510

Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg
515 520 525

Glu Val Asp Ser Ser Ala Ala Gln Arg Gly His Ser Leu Leu Ser
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Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg
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<210> 110

<211> 21

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

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tagggaccocg gctttggcct tcaggtctcc tagcagcggg gaaaaggaat 200
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<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

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 Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu
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 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
 35 40 45
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala
 50 55 60
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
 65 70 75
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 80 85 90
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
 95 100 105
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro
 110 115 120
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln
 125 130 135
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro
 140 145 150

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln	425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu	
				440					445					450	
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr	
				455					460					465	
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly	
				470					475					480	
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe	
				485					490					495	
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr	
				500					505					510	
Gly	Ile	Gln	Glu	Ser											
				515											

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

cccaacccaa ctgtttacct ctgg 24

<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

gccaccctac ctcaaaaact gaaggaggtt ggntattcaa cgcataatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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gggctcagga ggaggaagga ggaccgcgtg gagaatgcct ctgccctgga 150
gccttgcgct cccgctgctg ctctcctggg tggcaggtgg ttccgggaac 200
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gagtgcgtgg gaccaaaca atgcagatgc ttccaggat acaccgggaa 400
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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
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Gly Lys Lys Gly Asn Glu Glu Lys
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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ggccgagtgg cagggacgac gccagaatg ggagctgact gatatggtgg 150

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 aagatatact tgttttgcgc cttagacctga ccgacactgg tcccatgaa 350
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 caacaatggg ggaatgtccc agcgtttctct gtgcatggat accagcttgg 450
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 acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550
 tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600
 actgtgctag caagcatgct ctccgggggtt tttttaatgg ccttcgaaca 650
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 ctataggcaa taatggagac cagtccaca agatgacaac cagtcgttgt 800
 gtgcggctga tgtaatcag catggccaat gatttgaaag aagtttggat 850
 ctcagaacaa cttttcttgt tagtaacata tttgtggcaa tacatgcaa 900
 cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950
 ttttaagagt gtgtggatgc agactcttct tattttaaaa tctttaagac 1000
 aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050
 aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100
 actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150
 gaatgaaata aaaaataaat aataaaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
			20					25					30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35					40					45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50					55					60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	
					65				70					75	
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	
				80					85					90	
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	
				95					100					105	
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	
				110					115					120	
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	
				125					130					135	
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	
				140					145					150	
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	
				155					160					165	
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	
				170					175					180	
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	
				185					190					195	
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	
				200					205					210	
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	
				215					220					225	
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	
				230					235					240	
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	
				245					250					255	
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	
				260					265					270	
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	
				275					280					285	

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
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ggcaggggtt tggggctggg ggagcatgtg ctgggacagg acagcatcct 100
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgtaggttg cctgcggaca cgctgggctt ctgtcctgat gctgctgagc 200
tccctgggtg ctctcgctgg ttctgtctac ctggcctgga tccctgttctt 250
cgtgctctat gattttctgca ttgtttgtat caccacctat gctatcaacg 300
tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 350
gctaagaggc actgagccct caaccaagc caggctgacc tcctctgctt 400
tgctttgggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450
ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500
aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctgggtg 550
gcagacacct gggctctcac tgctgccac tgctttgaaa aggcagcagc 600
aacagaactg aattcctggg cagtggctct gggttctctg cagcgtgagg 650
gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgcc 700
agggcctata accactacag ccagggtcca gacctggccc tgctgcagct 750
cgccacccc acgaccaca caccctctg cctgccccag cccgccatc 800
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ctgatgcacc agggacagct ggactgtggc ggagccctgg tgtcagagga 1350
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 aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450
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 gcccgtagcc ctctggggc ctagggcctg cagccggctg catgcagctc 1700
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 gaggactggg tcagcagttt ggactggcag gtctacttcg ccgaggaacc 1950
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 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300
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 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp
				320					325					330

Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly
				335					340					345

Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys
				350					355					360

Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly
				365					370					375

Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly
				380					385					390

Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu
				395					400					405

Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys
				410					415					420

Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp
				425					430					435

Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln
				440					445					450

Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu
				455					460					465

His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met
				470					475					480

Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu
				485					490					495

Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu
				500					505					510

Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg
				515					520					525

Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser
				530					535					540

Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu
				545					550					555

Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser
				560					565					570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cggggcgcgc cgggccccca ttcgggccgg gcctcgctgc ggcggcgact 50
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ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150
gatgctgctg cggcggggca gccctggcat ggggtgtgat gtgggtgcag 200
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cctgaagacc cagtgtgggc actgtggggc accgatgcca cctgtgctg 300
ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350
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gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450
ggcacagggc aacgcattcc tgaggctgca gcgcgtgctg gtggcgagac 500
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gtcagcctgc aggtggcgc tccctactcg aagcccagca tgaccctgga 600
gcccacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650
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atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950

attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met	Leu	Arg	Arg	Arg	Gly	Ser	Pro	Gly	Met	Gly	Val	His	Val	Gly
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			20						25					30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
			35						40					45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
			50						55					60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
			65						70					75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
			80						85					90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
			95						100					105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
			110						115					120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
			125						130					135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
			140						145					150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
			155						160					165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp
			170						175					180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
			185						190					195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
			200						205					210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
			215						220					225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgccaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
ttcgtgaccc ttgagaaaag agttggtggt aaatgtgcc cgtcttctaa 50
gaaggggggag tectgaactt gtctgaagcc cttgtccgta agccttgaac 100
taagttotta aatctatgaa gtcgagggac ctttcgctgc tttttaggg 150
acttttttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250
agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300
aaggaggggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350
ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcatactgg aggcctctcaa aggttgggac cagggcctga 450
aaggaatgtg tgtaggagag aagagaaagc tcatactcc tctgctctg 500
ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550
atttaatat gatctctgg agattcgaaa tggaccaaga tcccatgaat 600
cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650
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gagttataga gatacatcta cctttttaat atagcactca tttttcaaga 850
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<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met	Arg	Leu	Phe	Leu	Trp	Asn	Ala	Val	Leu	Thr	Leu	Phe	Val	Thr
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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30

Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35					40						45

Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50					55						60

Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65					70						75

Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80					85						90

Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
			95					100						105

Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110					115						120

Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125					130						135

Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140					145						150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
			155					160					165	
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
			170					175					180	
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
			185					190					195	
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
			200					205					210	

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgcc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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cagagatgcc tggctacctc gccctgcctt cagcctcaag gggctcagtc 200
tttttttctc ttggtgccca ccaggacgga gcatggaggt cacagtaact 250
gcccacctca acgtctctaa tggctctgac gcccgctgc cctgcacctt 300
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aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450
agggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500
cggaggatga ggggatttac aactgctaca tcatgaaccc cctgaccgc 550
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 aagtgacaat tgtaggccag gcacagtggc tcacgctgt aatcccagca 1950
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 ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtggtgg 2050
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 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
1				5					10					15

Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcagc gggctcagtc tctttttctc tttggtgcca 200
 ccaggacgga gcatggaggt ccacagtacc tgnccacct caacgtctc 250
 aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttctcc agttccgcat gaagatcatt aacctgaagc 400
 tggagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450
 gatgtgtcgg tgatgtgag aaactgacag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<212> 56, 123
<213> unknown base

<400> 152
tcacgggggt catctctttt ttcttttggg gccaccagg acggagcatg 50
gaggtnacac tacctgccac cctcaacgtc ctcaatgggt ttgacgccg 100
ctgacctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
cctgaactg gatttaccag gagtgcacac actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300
tcgggtgatg tgagaaacgt gcagccggag gatgagggga ttacaaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgccctgcctt gcaccttcaa ctccctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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gggtgctcc cggatggcct cctgttccctc ttgtgtgtgc taatgtgtct 100

cgcggaacca gcgtcccggt ccggacgtca cccccagtg gtgtgggtcc 150

ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200

gtgcactacc tctgtcccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgtgtgtgc ctgtcatcat tgactgtgtg attgacaata 300

tcaggctggt ttacaacaaa acatccagggt ccaccagtt tctgatggt 350

gtggatgtac gtgtccctgg ctttgggaag accttctcac tggagtccct 400

ggaccccagc aaaagcagcg tgggttccta ttccacacc atggtggaga 450

gccttggtgg ctggggctac acacgggggtg aggatgtccg aggggtcccc 500

tatgactggc gccgagcccc aaatgaaaaa gggccctact tctggccct 550

ccgcgagatg atcgaggaga tgtaccagct gtatgggggc ccgtggtgc 600

tggttgcccc cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650

cagccgcagg cctggaagga caagtatata cgggccttcg tgtcactggg 700

tgcgccctgg gggggcgtgg ccaagacctt gcgcgtcctg gcttcaggag 750

acaacaaccg gatcccagtc atcgggcccc tgaagatccg ggagcagcag 800

cggtcagctg tctccaccag ctggctgtgt ccctacaact acacatggtc 850

acctgagaag gtgttcgtgc agacacccac aatcaactac aactgcggg 900

actaccgcaa gttcttccag gacatcggct ttgaagatgg ctggctcatg 950

cggcaggaca cagaagggtt ggtggaagcc acgatgccac ctggcgtgca 1000

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atgctgtataa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp	
				80				85					90	

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
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245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr		
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln		
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu		
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys		
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu		
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp		
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln		
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser		
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu		
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacggggc ctacttcttg gccctccgag agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cggacgcgtg ggcggacgag tggggcggcg gcagcggcgg cgacggcgac 50
atggagagcg gggcctacgg cgcggccaag gcgggcggtt ccttcgacct 100
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgac gtgtgcttgg 150
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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				20					25					30
Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val
				95					100					105
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

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<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 166

ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

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<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
cctgggtgcc ctgtttgtgc tgetggccct gctcgtgctg gcttcggcgg 250
gggtgtact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300
caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350
tcttaccgcg cgggaatcta gtgccttccg cagtgaacc gccaaagccc 400
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ctggttcatt ctcaaattcc ccgagcaccg ccggctgatg ctgagccccg 550
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 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 169
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 Gly Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala
 20 25 30
 Cys Glu Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val
 35 40 45
 Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly
 50 55 60
 Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val
 65 70 75
 Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe
 80 85 90
 Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu

95	100	105
Thr Ala Lys Ala Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser Thr	
110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly	
125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro	
140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu	
155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val	
170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile	
185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu	
200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg	
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu	
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr	
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly	
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg	
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala	
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val	
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln	Ala Cys Glu Val Asn Leu	
320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro	
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His	
350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe Asp	
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln	

	380	385	390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile
	395	400	405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly
	410	415	420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly
	425	430	435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro
	440	445	450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys
	455	460	465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys
	470	475	480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile
	485	490	495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly
	500	505	510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe
	515	520	525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro
	530	535	540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu
	545	550	555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly
	560	565	570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu
	575	580	585
Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala	Asp
	590	595	600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser	Met
	605	610	615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp	Gln
	620	625	630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg	Leu
	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp	Val
	650	655	660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala	Val

665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly		
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser		
785	790	795
Trp Ile Gln Gln Val Val Thr		
800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 170
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 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200
 tgtttctgtga atggactctg tgccctgcc tgtgatgggg tcaaggactg 250
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 ccgcctcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
 actgcccccc tgcaaagcag ggccacctc ctggactcag agagcccagg 1300
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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ccttctctgc 100

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<210> 178
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
350

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

cggacgcgtg ggaggacgag tgggcctggg caagggccgg ggccgcgggc 50

cgagccacct ctccccctcc cccgcttccc tgtcgcgctc cgtcggtgg 100
acgcgctgga ggagtggagc agcaccgggc cggccctggg ggtgacagt 150
cggcaaagtt tggcccgaaag aggaagtggc ctcaaaccac ggcaggtggc 200
gaccaggcca gaccaggggc gctcgctgcc tgcggggcgg ctgtaggcga 250
gggcgcgccc cagtgcgag acccggggct tcaggagccg gccccgggag 300
agaagagtgc ggcgccggac ggagaaaaca actccaaagt tggcgaaagg 350
caccgccccct actcccgggc tgcgcgcgcc tccccgcccc cagccctggc 400
atccagagta cgggtcgagc cggggccatg gagccccct ggggaggcgg 450
caccaggag cctgggcgcc cggggctccg ccgcgacccc atcggtaga 500
ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
gttgccacc ctctctctcc tctctcttg aggcgctctg gccatccag 600
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gagattgtgc agcagcaggc accccttcc tacgggcagc tcattgccc 2050
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actcagtgt gggcaacctg cgttctctgc tacagatctt acgccaggat 2150
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gatgcagcgc ctggtacgcc gtctccgccg ctggggcttg ctccctcgaa 2250
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taagtgtccc tcaggcaggg agagggtca cagagtctcc tctgtactg 2900

gccatggcca gacaccccag tcccttcacc accaactgct ccccacgcca 2950
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
 ggtctggaca ctccatcctt gccaaaacctc tacccaaaag tggccttaag 3050
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctacacaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200
 ccagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr			

185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200					205					210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					

470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser 485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp 500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu 515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly 530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg 545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn 560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser 575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg 590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro 605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala 620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro 635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly 650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro 665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp 680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu 695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr 710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtcacca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgctgtctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagacctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtg ctgtgggtc tgcagacgg atggataacg tgcagccgaa 150
 aataaaacat cgcctcttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tggggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gcccctgaac catatatgtg tatcaactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgcacgatta atgaagtgg 350
 ttttttggc tttgttgat attatcaact cactggtaac aacagtattc 400
 atgtcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
 agttggtgga ggggtgttg cactgtgac agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggctcttac 550
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
 tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
1				5					10					15
Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
 140 145 150

Val Leu

<210> 191
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 212, 234, 487
 <223> unknown base

<400> 191
 gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
 ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
 ctgctgctgg gctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
 catcgccctt tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
 ggcaactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
 aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
 atacttttat atgtactcag acttgatcga ttaatgaagt gggtattttg 350
 gcctttgctt gatattatca actcactggg aacaacagta ttcattgtca 400
 tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450
 ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 192
 cgttttgcag aacctactca ggcag 25

<210> 193
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtctg tgtgtgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgtgagc cgcggctgcc ggacgggacg 50
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcattgggcg 100
cactggcccg ggcgtgtctg ctgcctctgc tggcccagtg gctcctgcgc 150
gccgccccgc agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200
cgcggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccttg 250
ccgagcgcca cgccgacggc ttggcgctcg ccttgagacc tgccctggcg 300
tccccgcgg gcgccgcaa cttcttgccc atggtagaca acctgcaggg 350
ggactctggc cgcggctaact acctggagat gctgatcggg accccccgc 400
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450
ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550
gctggacggg ctctgttggg gaagacctcg tcaccatccc caaaggcttc 600
aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700
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acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagccgg 800
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
acagtggcac caagctgctg cgcctgcccc agaaggtgtt tgatgcgggtg 1050
gtggaagctg tggccccgcg atctctgatt ccagaattct ctgatgggtt 1100
ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttggg 1150
cttacttccc taaaatctcc atctacctga gagatgagaa ctccagcagg 1200
tcattccgta tcacaatctt gcctcagctt tacattcagc ccatgatggg 1250
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atgcgctggg gatcgggtgc acggtgatgg agggcttcta cgtcatcttc 1350
gacagagccc agaagagggt gggcttcgca ggcagcccc gtgcagaaat 1400
tgcagggtgt gcagtgtctg aaatttcggg gcctttctca acagaggatg 1450
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atagccaggc ctgacctcaa gcaaccatga actcagctat taagaaaatc 1700
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caccgctctt caatctctgt tctgtccca gatgccttct agattcactg 1800
cttttggatt ctgattttc aagctttcaa atcttccta cttccaagaa 1850
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
<211> 518
<212> PRT.
<213> Homo sapien

<400> 196
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln
1 5 10 15
Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
20 25 30
Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
35 40 45
Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
50 55 60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala				65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg				80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu				95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly				110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser				125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr				140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile				155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile				170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly				185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser				200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro				215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala				230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu				245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu				260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly				275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala				290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val				305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro				320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp				335	340	345

Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	350	355	360
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	365	370	375
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	380	385	390
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	395	400	405
Val	Ile	Gly	Ala	Thr	Val	Met	Glu	Gly	Phe	Tyr	Val	Ile	Phe	Asp	410	415	420
Arg	Ala	Gln	Lys	Arg	Val	Gly	Phe	Ala	Ala	Ser	Pro	Cys	Ala	Glu	425	430	435
Ile	Ala	Gly	Ala	Ala	Val	Ser	Glu	Ile	Ser	Gly	Pro	Phe	Ser	Thr	440	445	450
Glu	Asp	Val	Ala	Ser	Asn	Cys	Val	Pro	Ala	Gln	Ser	Leu	Ser	Glu	455	460	465
Pro	Ile	Leu	Trp	Ile	Val	Ser	Tyr	Ala	Leu	Met	Ser	Val	Cys	Gly	470	475	480
Ala	Ile	Leu	Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Leu	Pro	Phe	Arg	485	490	495
Cys	Gln	Arg	Arg	Pro	Arg	Asp	Pro	Glu	Val	Val	Asn	Asp	Glu	Ser	500	505	510
Ser	Leu	Val	Arg	His	Arg	Trp	Lys								515		

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

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<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199
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ggatgtagcc agcaactgtg 20

<210> 200
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<212> DNA
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gccttggtc gttctcttc 19

<210> 201
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<220>
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ggtcctgtgc ctggatgg 18

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gacaagacta cctccgttgg tc 22

<210> 203
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<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

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cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

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<212> DNA
<213> Homo sapiens

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taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30
Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45
Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60
Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	80	85	90
Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	100	105
Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	115	120
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	130	135
Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	145	150
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	160	165
Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe	170	175	180
Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	190	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	205	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	220	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	235	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	250	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	265	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	280	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	295	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro	305	310	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	325	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	340	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcattggcc ttggacttgg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

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<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20					25						30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
			35					40						45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
			50					55						60
Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
			65					70						75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
			80					85						90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
			95					100						105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
			110					115						120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
			125					130						135

Cys Gly Pro Pro	Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr	425	430	435
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala	440	445	450
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val	455	460	465
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly	470	475	480
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met	485	490	495
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr	500	505	510
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg	515	520	525
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu	530	535	540
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp	545	550	555
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser	560	565	570
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu	575	580	585
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp	590	595	600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu	605	610	615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln	620	625	630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu	635	640	645
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser	650	655	660
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala	665	670	675
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg	680	685	690
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr	695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 212

gaagggacct acatgtgtgt ggcc 24

<210> 213

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 213

actgaccttc cagctgagcc acac 24

<210> 214

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggg gtccagcgcc cagaatgcgg cttctgggtc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

gcggggttca aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aaggggtggga tctctttctc 200

tgcgtgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggg gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

acccctgtgga acctcaccct gcaagaagct ggggagtaact ggtgtggggat 350
cgaaaaaacgg ggccccgatg agtcttttaact gatctctctg ttogtctttc 400
caggaccctg ctgtctctccc tcccctttctc ccaccttcca gctcttggt 450
acaacacgcc tgcagcccaa ggcaaaagct cagcaaaccc agcccccagg 500
attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550
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 gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050
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 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550
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 tctttttaca gagcaattat cttgtatata caactttgta tcttgccttt 2650
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5				10					15	

Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
			20					25					30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
			35					40					45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50	55	60
Cys Ser Gly Thr	Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met		
	65	70	75
Lys Gly Arg Val	Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu		
	80	85	90
Ile Val Thr Leu	Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr		
	95	100	105
Trp Cys Gly Val	Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile		
	110	115	120
Ser Leu Phe Val	Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser		
	125	130	135
Pro Thr Phe Gln	Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala		
	140	145	150
Lys Ala Gln Gln	Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu		
	155	160	165
Tyr Pro Ala Ala	Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu		
	170	175	180
Ala Pro Pro Leu	Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr		
	185	190	195
Ser Gln Tyr Thr	Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro		
	200	205	210
Ala Gly Ser Ser	Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala		
	215	220	225
Glu Asp Thr Ser	Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg		
	230	235	240
Val Ser Ile Pro	Met Val Arg Ile Leu Ala Pro Val Leu Val Leu		
	245	250	255
Leu Ser Leu Leu	Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His		
	260	265	270
Leu Leu Leu Trp	Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln		
	275	280	285
Arg Asn Glu Lys	Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys		
	290	295	300
Glu Ala Pro Ser	Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro		
	305	310	315
Pro Leu His Thr	Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val		
	320	325	330
Ser Ala			

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggt gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacac 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
cagtgtagaaa gaaccagtggt tctcgtctctg ttgccagggc tagagtgtac 150
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcaactcaagc 250
cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
ccgccggcat agaagccagg agcaggggctc tcagaaggcg gtggtgccca 400

gctgggatac tgttgttggc cctgggtctgt ctgctcagct gcttctacc 450
 ctccagtgag gccaaactct acggctggtg tgaactggcc agagtgtac 500
 atgacttcgg gctggacgga tacgggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tgttggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta cctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggcccgg cgcccgcggc ggcaccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tctcgtcttt cgcggtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaagctgt cgtcggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc cgcggtgccc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
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gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttcagtg ggtaaggatg 500
ctctgacaac atcgccatcg gtgtggcctt ctacacagtcg tttgtggatg 550
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atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700
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gctgtgcctt tgcagtcatt ccagagtcac ctttcacaga gctgttcctc 1900
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
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 ctgtgccttt gcagtcattc ccagagtcac ctttcacaga ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 227
 gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgtttaaat tatcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgatttgtca agtgcgggca gtgcacggcg ctggtggagt : 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

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gtcccgagga ggccccggga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctgggtgtc ctgggcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggctccacg gagcgcgcg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
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cgcaggcgaa gctgatggag caggagagcg cctgcggga actgcgtgag 450
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gtgctcacc tccctggctc ctggagctga ttgcacaaaga gttttttct 1050
tctcatcca ccgtgtgtga gtctcagaaa caattggccc aacatagccc 1100
tgtccagccc agtgcctggg ctctgggacc tccatgcga cctcactcta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
 ctctcgctc cccgtgatat gctccactt ctctccctaa ccaagggttag 1250
 gtgaactgagg actggagctg ttgggttttc tgcattttc caccaaaactg 1300
 gaagctgttt ttgcagctg aggaagcctc aataaatatt tgagaaatga 1350
 aaaaa 1355

<210> 231
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 231
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
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 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
 20 25 30
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
 35 40 45
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
 50 55 60
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
 65 70 75
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
 80 85 90
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
 95 100 105
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
 110 115 120
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
 125 130 135
 Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg
 140 145 150
 Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys
 155 160 165
 Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser
 170 175 180
 Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp
 185 190 195
 Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly
 200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
275 280 285

Ile Cys Glu Lys Arg His Asn Cys
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgatcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

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<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

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			20						25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
			35						40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
			50						55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
			65						70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
			80						85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
			95						100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val
			110						115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
			125						130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
			140						145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
			155						160					165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala	170	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	320	325	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcaatgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 239
 cagcccttc tctctcttc tccc 24

 <210> 240
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 240
 qcagttatca gggacgcact cagcc 25

 <210> 241
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 <212> DNA
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 <400> 241
 ccagcgagag gcagatag 18

 <210> 242
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 <400> 242
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 <210> 243
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 243
 cagcccttc tctctcttc tcccagctcc tatctgcctc tc 42

 <210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtgggtc aaagaagctc ctaaagcttg 300
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 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20						25					30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35						40					45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50						55					60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65						70					75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80						85					90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95						100					105
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala
			110						115					120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly
			125						130					135

Asp Thr Val Tyr	Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
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<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgccgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

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<223> Synthetic oligonucleotide probe

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cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 252
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<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

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<211> 545
<212> PRT
<213> Homo sapiens

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Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
35 40 45
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
50 55 60
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
65 70 75
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
80 85 90
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
95 100 105
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
110 115 120
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro		140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg		155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu		170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu		185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg		200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val		215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met		230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser		245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val		260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp		275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala		290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp		305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser		320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His		335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile		350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala		365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg		380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg		395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp		410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
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<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257

gaacgggtaca agtgggtggg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

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<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met	20	25	30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp	50	55	60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr	65	70	75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe	80	85	90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile	95	100	105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val	110	115	120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe	125	130	135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp	140	145	150	
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly	155	160	165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro	170	175	180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu	185	190	195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys	200	205	210	
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro	215	220	225	

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgccca ccattcaaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcato acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc totacatctt aagagcccag gtaatagaca 400
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tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600
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aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650
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atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
tatagtcaga gaaattttca tgaattatc catgaagtat tgtttccttt 2850
atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys	
				20					25					30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	
				35					40					45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	
				50					55					60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
				170					175					180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser	290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile	305	310	315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr	320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu	335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln	350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr	365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly	380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg	395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly	410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp	425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln	440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp	455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu	470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp	485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser	500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln	515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu	530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn	545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val	560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	
				575					580					585	
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	
				590					595					600	
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	
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Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	
				620					625					630	
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	
				635					640					645	
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
				650					655					660	
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
				665					670					675	
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
				740					745					750	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
				755					760					765	
Ser	Ala	Val	Gln	Ser	Asn	Asn									
				770											

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaaacttt cagatgttaa tgacaataag cctatatatta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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cccgcccttaa cttcctccgc ggggccccagc caccttcggg agtcggggtt 150

gcccacctgc aaactctcgg ccttctgcac ctgccacccc tgagccagcg 200
cgggcccccg agcgagtcac ggccaacggc gggctgcagc tgttgggctt 250
cattctcgcc ttctgggat ggatcggcgc catcgtcagc actgccctgc 300
cccagtgag gatttactcc tatgcggcgc acaacatcgt gaccgccag 350
gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400
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ttgcaggtct ggctatttta gttgccacag catggtatgg caatagaatc 650
gttcaagaat tctatgacct tatgaccca gtcaatgcc ggtacgaatt 700
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ctcaatatag gaggaagat tttccattt gtattactgc ttcccattga 1100
gtaatcatac tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150
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cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
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ccttatatac atatgtaaca gtcaaatatc atttactctt cttcattagc 1350
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ataatcttat agcaattgca tegtatttaa gcccttattt gttttgtgtt 1500
tcattggtct ctatctcctg aatctaacac atttcatagc ctacatttta 1550
gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600

tttttctgca tgaacaaaagt gataaattcc tgttgacett cccacacaaat 1650
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 tgctagacct tctggagtga taatctggtg acaaatattc tctctgtagc 1950
 tgtaagcaag tcacttaatc tttctacctc tttttctat ctgccaaatt 2000
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 tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150
 acacgtacct tcctgtgatt cactgccttc ctctctctac cagtctattt 2200
 ccactgaaca aaacctacac acataccttc atgtggttca gtgccttcct 2250
 ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300
 gtggctcagt gccttctct ctctaccagt ctatttccat tctttcagct 2350
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 gatgttgtgg ggatccagtg agatagaata catgtaagtg tggttttgta 2650
 atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

Met	Ala	Asn	Ala	Gly	Leu	Gln	Leu	Leu	Gly	Phe	Ile	Leu	Ala	Phe
1					5				10					15

Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

	20	25	30
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala	35	40	45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly	50	55	60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser	65	70	75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu	80	85	90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met	95	100	105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val	110	115	120
Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val	125	130	135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp	140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu	155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala	170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr	185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr	200	205	210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt cchgcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
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 tgatgggtgtt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acantctat 450
 gacctatga cccagtcac tgccaggtac gaatttggtc aggcctctct 500
 cactggctgg gctgctgctt ctctctgctt tctgggaggt gccctacttt 550
 gctgttcttg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
 tccagctgtt gggettcatt ctccccttcc tgggatggac cggcgcccat 100
 cntcagcaact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
 acatcgtgac cgcgccaggcc ntgtacgagg ggctgtggat gtcttgctg 200
 tcgcagagca ccgggcagat ccagtgcaca gtctttgact cccttgctga 250
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300
 ctctggggag tgatagcaat cttntggcc accgttgtnn ntgaagtga 350
 tgaagtgcctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
 gggggcgcga tatttcttct tgcaggctctg gctatttttag ttgccacagc 450
 atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

gggcccgcacc attatccaac cgggntcact gttgggtcat ctccctcctg 50
gatgaanccg gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cnttgccctg atggtgggtg 250
gcctcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgggaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgccagg tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450
cccagtcatt gccaggtacg aatttggta ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctccct cctggatgga tcgncacc gtcacattgc ctcccccan 50
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgtc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
cnnghnntct atgaccctat gaccccagtc aatgccaggt acgaatttgg 450

tcaggtctctc ttcaactggct gggtctgtgc ttctctctgc cttctgggag 500

gtgcctact ttgtgttcc tgccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

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gcagcacatt ncaagcaacc ccttgccttg aagggtggtg ncatccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gacctatga cccagtcaa 300

tgccaggtag gaatttggtc aggtctctct cactggtctg gctgctgctt 350

ctctctgctt tctgggaggt gccctacttt gctgttctg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

agcaatgccc tgccccagt ggaggattaa ttccctatgnt ggggacaaca 50

ttgtgaacgc ccaggccatg tacggggggc tgtggatgct ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcatcttcc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaa acgatgaggt gcagaagatg aggatggctg tcattggggg 300

gcgatattt cttnttgcat gtctggctat tttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttggtea ggctttnttc actggetggg ctgetgettn 450

tttctgcctt ntgggaggtg cctantttg ctgttcttgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataaggggg gcgcgatatt tttctttgca ggtntgggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttggtc aggcctctntt cactggntgg 150

getgetgctt ctntnngcct tntgggaggt gccctacttt gctgttcttg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

ttcttgggat ggatccgccc ccactntcac atgccctgcc cnttggagat 50

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gggctgtgga atgtcttgcg tgtcccagag caccgggcag atccagtga 150

aagtctttga ctcttctgtg aatctgagca gcacattga agcaacntg 200

ccttgatggg ggttggcacc ctcttgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtga tgaagtgcct ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350

gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcaactg getgggctgc tgettctctc tgccttcttg gaggtgcct 500

actttgtgt tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcattctgc ttcctgggat ggaatcggcg 50
ccatcgctcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtga aagtctttga ctcttgctg 200
aatctgagca gcacattgca agcaacctg ccttgatggg ggttggcacc 250
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcctt gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350
ggggcgcgat atttcttctt gcagggtctgg ctatttntag ttgccacagc 400
atgggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttgcctgt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283
<211> 2285
<212> DNA
<213> Homo sapiens

<400> 283
jcgtagcgtc agctgcgcgg gcacgcgggc ctgcacctcg cctccgccc 50
ctgcgcctgc acgcggtaga cgcaccccc cctccagcgc gccaccccg 100
tagaggaccc ccgcccgtgc ccgcaccggt ccccgcttt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200
ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250
ggtcctgagc ctgcagccgc agcacgagct caaatccga ggtcccttca 300
ccgatgttgt caccaccaac ctaaagcttg gcaaccgcac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
caacagcggg atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat ccaatgaga aaagtaaaca caagtttatg 500
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950
aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattgggtg 1000
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

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ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
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ctttattaat gacaagggaa accatgagta atgccacaat ggcattattgt 1250
aaatgtcatt ttaaaccattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350
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acgtggccca ctcccgccc aggtgcttt cctgtcttc agttctgtcc 1450
aagccatcag ctcttgga ctgatgaaca gagtcagaag cccaaaggaa 1500
ttgcactgtg gcagcatcag acgtactcgt cataagttag aggcgtgtgt 1550
tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttact 1600
taaagggacc aagctaaatt tgtattgggt catgtagtga agtcaaactg 1650
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatct 1700
catgttttct tattgtcaca agagtacagt taatgctgcg tgcgtctgaa 1750
ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800
ctctggagag tctggtcatg tggaggtggg gtttattggg atgctggaga 1850
agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950
tgaagagtag tcagttctct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcggcca ggtccaagtc tgagcctgac ctccccttgg 2050
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
gcgagggcac cagcagttgt ggggtggggag caaggggaaga gagaaaactct 2150
tcagcgaatc cttctagtag tagttgagag ttgactgtg aattaatttt 2200
atgccataaa agaccaacct agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255
<223> unknown base

<400> 285
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tonagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnnttagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
cttctagtac tagttgagag ttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 73, 97
<223> unknown base

<400> 286
tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaatgaca ccttccctcg cctgttggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcaactta agggaaccaag ctaaattgta ttgggttcag tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
tcattctatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctgggtattgc tgctggaggg ctg 543

<210> 287
<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
ccctgggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50
ctttagtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
ggtggcccat tcccggccca ggctgctttc cggtnntcag ttctgtccaa 50
gcatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaatgca tatttaantt atttaatgta ttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttgggtg aactggtatt gctgctggag ggctgtgggc tctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcacagaacg 100
 tactcgatc aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gtcaacttaa agggaccaag cttaaattgt 200
 attggttcac gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
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<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

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 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
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 atgcatattt aanttattta atgtatttca tntcatgttt tottattgtc 550
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 gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
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 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
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<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200
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atttttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350
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<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

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20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu		
35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr		
50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu		
65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn		
80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu		
95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg		
110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp		
125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu		
140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu		
155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly		
170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser		
185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala		
200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu		
215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln		
230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys		
245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp		
260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala		
275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys		
290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp		

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 297
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<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
 catcggtccc gtgaatccag aggc 24

<210> 299
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
 gaaggaggcc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869
<212> DNA
<213> Homo sapiens

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tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tectgagttc 200
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<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30

Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45

Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75

Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90

Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105

Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120

Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe	
				425					430					435	
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val	
				440					445					450	
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp	
				455					460					465	
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro	
				470					475					480	
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro	
				485					490					495	
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln	
				500					505					510	
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser	
				515					520					525	

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

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<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
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Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20						25				30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
			35						40				45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
			50						55				60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
			65						70				75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
			80						85				90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 20, 34, 62, 87, 221, 229
<223> unknown base

<400> 304
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gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
qaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaattat ctgcctggct t 521

<210> 305
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 305
ccaggaaatg ctccaggaag agcc 24

<210> 306
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 306
gcccattgaca ccaaattgaa gagtgg 26

<210> 307
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggg tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgtg cctggagaat cctccgctgc cgtcggtcc 50

cggagcccag ccttttcta acccaaccca acctagccca gtcccagccg 100

ccagcgctg tccctgtcac ggaccccagc gttaccatgc atcctgcctg 150

cttccatccc ttaccgacc tcagatgtc cttctgtc ctggtaactt 200

gggtttttac tctgtaca actgaaataa caagtcttg tacagagaat 250

atagatgaaa ttttaaaca tgctgatgt gcttagtaa atttttatgc 300

tgactggtgt cgtttcagtc agatgttgca tccaatttt gaggaagctt 350

ccgatgtcat taaggaagaa ttccaaatg aaatcaagt agtgtttgcc 400

agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450

caaataccca accctcaaat tgtttcgtaa tgggatgat atgaagagag 500

aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550

caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600

tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650

cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700

tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750

tggcgacaac ataatttaca aaccaccagg gcattctgct ccggatatgg 800

tgtacttggg agctatgaca aattttgat tgacttaca ttggattcaa 850

gataaatgtg ttctcttctg ccgagaaata acatttgaaa atggagagga 900

attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950

atacagaaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000

agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100

ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150

ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200

actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccctccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gctttaaaaa cttgaaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
 1 5 10 15
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
 20 25 30
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
 35 40 45
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
 50 55 60
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
 65 70 75
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
 80 85 90
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
 95 100 105
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
 110 115 120
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
 125 130 135
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
 140 145 150
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
 155 160 165
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg
 170 175 180
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 48

<223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtnnttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccccttcccta acccaaccca acctagcccn gtcccagccg 150
ccagcgccctg tccctgtenc ggancccage gtnaccatgc atcctgccgt 200
cttccatccc ttaccgcacc tcagatgctc ccttctgctc ctggtaactt 250
gggtttttac tccgtgaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactgggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
<211> 19
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

cagactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttctcta tccttaaccg acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgtgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

ccctcttgg catatcatat ttggagggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttgggtga gctottagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaaa 500

tgaagggtat ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatgggtat tacgtataaa ttaatatataa atgattacct ctgggtgttga 700
 caggtttgaa ctgcaacttc ttaaggaaca gccataatcc totgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 ctgttagggc tcattttggg ttcaattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950
 atacattttac aaaaataaaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt ctttaagcata agtaaacatg atataaaaaat 1100
 atatgctgaa ttacttgtga agaattgcatt taaagctatt ttaaatgtgt 1150
 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200
 ttctaactcg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323
<211> 477
<212> DNA
<213> Homo sapiens

<400> 323
attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgcccct cttggcatat catatttggg ggtatatgag tagaccagtg 200
atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
tagcattttt ttactacctt tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgata agttacttta aaaaatg 477

<210> 324
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 325
caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagagggtg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttgggtgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttccctct 500
 aactctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
 gtttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
 ggagccctaca aatttgagag aatcatctct aagcaaaatg tcttatctgc 700
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgtc ctctcgggtga tggatttgc ttggatttgc tgtgcaactg 850
 ttgtacagc tgtggagcag tatgttccct ctgagaagct gattatctat 900
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
 caaataaagt tactcaaata tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10				15	

Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25					30

Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40					45

Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55					60

Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70					75

Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85					90

Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100					105

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaataca 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaattctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

cacactggcc ggatctttta gaggcctttg accttgacca agggtcngga 50
aaacagcaac aagctgagct gctgtgacag agggacaacag atggcggcgc 100
cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggccttggcc ggagggttcgg ggaccgcttc ggctgaagca 200
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
gacttaaate gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgccccggag gtggggcgcc gctggggccg gcccgcacgg gttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatggggccg cggctgggga ttcttgtttg 200
gcctcctggg cgcctgtgtg ctgctcagct cgggccacgg agaggagcag 250
cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cctttaaatc ctttggttc tggtaaggg 850
 acaagtgaag agaacacatt ttacagttgg ctagaaggtc tctgtgtaga 900
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950
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 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
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 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
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 acttctggaa atacttcatt aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350
 ttgtttttaa tgcgtctgtt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttataa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
 1 5 10 15
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30

Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe
320 325 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu
335 340 345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu
350 355 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys
365 370 375

Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp
380 385 390

Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr
395 400 405

Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu
410 415 420

Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu
425 430 435

Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile
440 445 450

Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln
455 460 465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100

nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150

ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200

caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250

attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300

tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtggttacc aaattngagc gccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcac ttcccttgca ttttgatgag aattcatttt 500
tttgctg 507

<210> 339
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
aagctgccgg agctgcaatg 20

<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgcttctta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac tttcgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 343

tgccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagagggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggactttctca tactggacag aaaccgatca ggcattggaac tcccccttct 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatgtt ggggggtggac agcgatggat 300

gctgggtggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca totcatctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agaggggtgtt ggcagtgtct ctgaagggtcc ataaaagaaa 550

aaagagaagt gtggttaagg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtta tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800

attccagcct caggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
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cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
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aaaataataa taataataat tcagactcct taccaggagt ccattgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe	1	5	10	15
Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro	20	25	30	
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val	35	40	45	
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala	50	55	60	
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg	65	70	75	
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His	80	85	90	
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn	95	100	105	
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly	110	115	120	

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
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ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagaggggac agaggccaga ggactttctca tactggacag aaaccgatca 150
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350
aggcgaccgg aggggggacg tttatcgtg cctgtaggg gggggccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcgtcactc acctgttctt gcccttggtg ttctt 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
aaagttacat tttctctgga actctcctag gccactcctt gctgatgcaa 50
catctgggtt tgggcagaaa ggaggggtgt tcggagcccg ccctttctga 100
gcttctctggg ccggtcttag aacaattcag gcttcgtgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatddd ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctacacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatt 400
tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
ccccagcagc tgggtgtcac tcaactgaagg tctgagtgat gatgtcactg 550
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ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttggtg 750
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caotgttcgt ctggaaaatg ggcgggtgc tccagtactc ctgttgccc 1050
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 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgtcctttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1					5				10					15

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
					20				25					30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttggaaa gaaacaatgt totaggtcaa actgagtcta 200
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250
tcattgtggtt tttctacgca ttgattccat gtttgotcac agatgaagtg 300
gccattctgc ctgccctca gaacctctct gtactctcaa ccaacatgaa 350
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attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450
tggatcccca gcagctggtg ctcaactcact gaaggtcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tcttgaagca tccctttaat 600
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cttncaacctg gttattgagc tggaggacct ggggccccag tttagattcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgtgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
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ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
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gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
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 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccttgga 800
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 tgggtgcccc catggctcgt gagactcccc ttcgaggatt gcaccgcgcc 1600
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20					25					30	

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35					40					45	

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
			50					55					60	

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
ggcgccctggt tctgcgcgta ctggctgtac ggagcaggag caagaggctg 50

ccgccagcct ccgccgccga gcctcggttcg tgtccccgcc cctcgctcct 100

gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag caccacgtc gcccccgga cgtcggtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggctccct gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggtcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg cttagagcaat tccagccatg gtgggtccca 550
atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600
gagtgggtgga tagccaaaaca acgagggaaa agggccatca cagacaatga 650
catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700
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 ttaaaaataa tgcactctaa aactgaaaga aaccttatca cattttcccc 2400
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 aaattctgat attgcacttc ttattttata taaaataatc cttaaatatc 2550
 caaatgaatc tgttaaaatg tttgattcct tgggaatggc cttaaaaata 2600
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 agtaaatgta gggtaagca tggacagcca gagctttcta tgtactgtta 2700
 aaattgaggt cacatatttt cttttgtatc ctggcaaata ctctgcagg 2750
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 attaccattg ccaactgattt tttttaaatg gtaaatgacc ttgtatataa 2850
 atattgccat atcatggtac ctataatggt gatatatttg tttctatgaa 2900
 aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950
 attttttttc tgctggtgga tttacatatt aaattttttc tgctggtgga 3000
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 363
 Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu
 1 5 10 15
 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
 20 25 30

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu	35	40	45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn	50	55	60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln	65	70	75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val	80	85	90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp	95	100	105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu	110	115	120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln	125	130	135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His	140	145	150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys	155	160	165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly	170	175	180
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile	185	190	195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly	200	205	210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser	215	220	225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys	230	235	240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu	245	250	255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His	260	265	270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser	275	280	285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg	290	295	300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala	305	310	315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
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ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100
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accgcgcgtg tggacgggtc caaatgcaag tgetcccgga agggacccaa 300
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

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 cgaggtcagg agcaactgct gcaccccaag ctgcagagca ccaagcgctt 450
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<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu
1 5 10 15

Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala
20 25 30

Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
35 40 45

Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
50 55 60

Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
65 70 75

Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
80 85 90

Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys
95 100 105

Arg Arg Val Tyr Glu Glu
110

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctgggggccc ctgctcctgc tgcg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

gccccaggga ctgctatggc ttcccttggc gttcaccccg gtctgcgtca 50
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caaaatccgg ggccaaagaa caccgttaac caatgagatc ttgggtccag 200
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 taagagactt tgt 3113

<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser			
				155					160					165			
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu			
				170					175					180			
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly			
				185					190					195			
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly			
				200					205					210			
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu			
				215					220					225			
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly			
				230					235					240			
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly			
				245					250					255			
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser			
				260					265					270			
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu			
				275					280					285			
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile			
				290					295					300			
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met			
				305					310					315			
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln			
				320					325					330			
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile			
				335					340					345			
Asp	Gly	Asp	Val	Ile	Pro	Asp	Asp	Pro	Gln	Ile	Leu	Met	Glu	Gln			
				350					355					360			
Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Ile	Met	Leu	Gly	Val	Asn	Gln	Gly			
				365					370					375			
Glu	Gly	Leu	Lys	Phe	Val	Asp	Gly	Ile	Val	Asp	Asn	Glu	Asp	Gly			
				380					385					390			
Val	Thr	Pro	Asn	Asp	Phe	Asp	Phe	Ser	Val	Ser	Asn	Phe	Val	Asp			
				395					400					405			
Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Thr	Leu	Arg	Glu	Thr			
				410					415					420			
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu			
				425					430					435			

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	
440		445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	
455		460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	
470		475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	
485		490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	
500		505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	
515		520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	
530		535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	
545		550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	
560		565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	
575		580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	
590		595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	
605		610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	
620		625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	
635		640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650		655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665		670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680		685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695		700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710		715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly
800 805 810

His Ser Thr Thr Arg Val
815

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ggcgatgttt gtgggtcgg gatgggtcca ggaagttaact ccttcttctt 100
ttgttggggt ctgggcaggg gccacagcaa gtggggcggt gtcaaactgt 150
cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtgg 200
gcacaggcag ttctcactg tggaatctga tgggcaatgc catggtgatg 250
accagttata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300
gtggaaccgg gtgccatgtt tcttgagaga ctgggagttg caggtgcact 350
tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400
atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450
ggacaaattt gtggggctgg gagtatttgt agacacctac cccaatgagg 500
agaagcagca agagcgggta ttccctaca tctcagccat ggtgaacaac 550
ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600
aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttctggtga 650
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ctactacttc ggcacctcct ccatcactgg ggaatcttca gataatcatg 800
atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850
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gaccccgcat tcccatggtt gtgcatgggg acatctaact ctggtctggg 1250
aagccacca cccagggca atgtgtgtgt gatgtgcctt tccctgcagt 1300
ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350

caaaatcaca gaacagaatt tcatagccca ggcggccgtg ttgtttgact 1400
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450
 taacaccaca ggctttctga ccaccattc gttgggtttt gcatttgacc 1500
 caaccctctg cctacctgag gagctttctt tggaaaccag gatggaaaact 1550
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 ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20				25					30	

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly			
				35					40					45			
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro			
				50					55					60			
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met			
				65					70					75			
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp			
				80					85					90			
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe			
				95					100					105			
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln			
				110					115					120			
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr			
				125					130					135			
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys			
				140					145					150			
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu			
				155					160					165			
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn			
				170					175					180			
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr			
				185					190					195			
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp			
				200					205					210			
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met			
				215					220					225			
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val			
				230					235					240			
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser			
				245					250					255			
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys			
				260					265					270			
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu			
				275					280					285			
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro			
				290					295					300			
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe			
				305					310					315			

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ccttggtcg tggcagcagt gg 22

<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

cactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

ccgagccggg cgcgcagcga cggagctggg gccggcctgg gaccatgggc 50

gtgagtgc aa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100

ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150

tggggctctgg ctcaagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

gaggtttaat taatgootgo agtctgacat gttcccgatt tgaggtgaaa 250
ccatgaagag aaaatagaat acttaataat gcttttcggo aaccgcttct 300
tgctgctgct ggccctggct gogctgctgg cctttgtgag cctcagcctg 350
cagttcttcc acctgatccc ggtgtggaat cctaagaatg gaatgagtag 400
caagagtcga aagagaatca tgcccgaccc tgtgacggag cccctgtga 450
cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500
gagcgcagca tgggaaggta tgcccccgat ctttttaage tggctctcagt 550
gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600
aaacaaagcg accagaaaatt gactgcactc tgggtggctaa caggaaaaccg 650
tatcacccaa aactggaagc ttccattagt cacatgtcaa aaggatccgg 700
agcctctttc gaaagccctt tgaactcctt gcctctttac ccaaataacc 750
cattgtgtga gatgggagag ctcacacaga caggagttgt gcagcatttg 800
cagaacggtc agctgctgag ggatatctat ctaaagaaac acaaactcct 850
gcccaatgat tggctctgcag accagctcta ttagagacc actgggaaaa 900
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tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggtaactt 1950
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gattctctgt tgcctatggc attccaaactt tttctctttg tttttgtcca 3100

gtgttgcat tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala
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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25				30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40				45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55				60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70				75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85				90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100				105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115				120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130				135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145				150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160				165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175				180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190				195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205				210	
Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220				225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235				240	

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

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<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln			
			20						25					30			
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val			
			35						40					45			
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala			
			50						55					60			
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe			
			65						70					75			
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile			
			80						85					90			
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn			
			95						100					105			
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu			
			110						115					120			
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu			
			125						130					135			
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met			
			140						145					150			
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn			
			155						160					165			
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu			
			170						175					180			
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val			
			185						190					195			
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu			
			200						205					210			
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr			
			215						220					225			
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro			
			230						235					240			
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu			
			245						250					255			
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp			
			260						265					270			
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp			
			275						280					285			

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
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Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
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<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

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<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

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cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgogg ccaagacgtg 200
 gatgttcttg ctcttgctgg ggggagcctg ggcaggacac tccagggaac 250
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 caagaaatac ctgtggttca gtccatccca caccctgtt acaacagcag 500
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	
				80					85					90	
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	
				95					100					105	
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	
				125					130					135	
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	
				140					145					150	
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	
				155					160					165	
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	
				170					175					180	
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	
				185					190					195	
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	
				200					205					210	
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	
				215					220					225	
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	
				230					235					240	
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	
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Ile	Gly	Ser	Lys	Gly											
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<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

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<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccagga tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccgcgcc ggccgcgcgc ccgcgcgcgc gccaggtga gcgctccgcc 150

cgcgcgcagg cccgcgcgcg gccgcgcgcc gccgcgcgcc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac caactgatcc cataaaacat 250

tcatactccc ggccggccgc gctgcgcgcg ccgcgcagc ccgcgcgcgc 300

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gcctgcgtat gctacaatga gcccaaggtg acgacaagct gccccagca 650

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 ttacagggtt ccggggcagc gtttgttcca gaacgcgcgc tcccaccag 2150
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 gacgacgtgg aataaagagc ttttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT
<213> Homo sapiens

<400> 400

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			20						25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
				35					40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
			50						55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
				65					70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
				80					85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
				95					100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
				110					115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
				125					130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
				140					145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
				155					160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
				170					175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
				185					190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
				200					205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
				215					220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
				230					235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
				245					250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
				260					265					270	

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser	Glu Val
275		280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys	Arg
290		295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr	Gly Pro
305		310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu	Pro Leu
320		325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys	Ala Ser
335		340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala	Leu Lys
350		355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly	Ser Gly
365		370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro	Gly Ser
380		385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser	Glu Pro
395		400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly	Cys Ser
410		415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln	Ala Gly
425		430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly	Ala Leu
440		445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala	Leu Val
455		460	465
Leu Trp Thr Val	Leu Gly Pro Cys		
470			

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgacct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400
gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550
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 attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650
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<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu
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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu
			20						25					30
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
			35						40					45
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150

Thr Thr Phe Pro	Leu Lys Asn Ala	Glu Asp Leu Asp	Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile	Ser Pro Asn Ser	Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp	Gly Arg Lys Tyr	Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg	Glu Glu Glu Ala	Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly	Gly Ser Pro Pro	Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val	Leu Asp Val Asn	Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr	Arg Val Gln Ile	Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val	Lys Val Ser Ala	Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile	Ser Tyr Ser Leu	Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe	Lys Ile Asn Pro	Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu	Asp Phe Glu Lys	Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg	Asp Ala Gly Thr	Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val	Ile Asp Val Asn	Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe	Thr Ser Pro Ile	Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu	Phe Ser Val Ser	Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser	Cys Ser Ile Gln	Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu	Asn Phe Tyr Thr	Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser	Arg Ala Glu Tyr	Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr	Pro Met Leu Ile	Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala
440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe Val	Arg Glu Asn Asn Ser
455	460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp Ser
470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp
485	490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp Asn
500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln
515	520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro Ala
530	535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala Asn
545	550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser Ala
560	565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr Leu
575	580	585
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn Ala
590	595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu Phe
605	610	615
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu Leu
620	625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val Lys
635	640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His Val
650	655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro Glu
665	670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr Leu
680	685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser Val
695	700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala Ala
710	715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 cggctgcacga ccgccccgcg tcctcgccgt cctcgccctg tggcaagtat 150
 tgctgtgggt gctgggactt ccgcgcgcgc ggcgtggaggt tgcagaggaa 200
 agtggctcgt tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
 ggctgtgtac ctgggtgagg aggagctcct gcctgaccgc atgggccagg 300
 acagggcagc agaagaggcc aatgcggctg tggggctgga cacccaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgcctggagga gggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgtcggagca 500
 cacttcctg acagagaaga ggagtattac acagagccag aagtggcggg 550
 atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
 ccccaaagggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
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 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
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 caataagcaa atgcaaaaat attcaatag 1379

<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val	
				20					25					30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	
				35					40					45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	
				50					55					60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	
				65					70					75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	
				80					85					90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	
				170					175					180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
				185					190					195	
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	
				200					205					210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
				215					220					225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
				230					235					240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	

	260		265		270
Ala Lys Pro Met	Ala Arg Phe Asn His	Thr Asp Arg Thr Leu Glu			
275	280	285			
Thr Leu Lys Ile	Phe Ile Phe Asn Gln	Thr Gly Ile Glu Ala Lys			
290	295	300			
Lys Asn Val Val	Val Thr Gln Ala Asp	Gln Ile Gly Pro Leu Pro			
305	310	315			
Ser Thr Leu Ile	Lys Ser Val Asp Trp	Leu Leu Val Phe Ser Leu			
320	325	330			
Phe Phe Leu Ile	Ser Phe Ile Met Tyr	Ala Thr Ile Arg Thr Glu			
335	340	345			
Ser Ile Arg Trp	Leu Ile Pro Gly Gln	Glu Gln Glu His Val Glu			
350	355	360			

<210> 411
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 411
 cacagagcca gaagtggcgg aatc 24

<210> 412
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 412
 ccacatgttc ctgctcttgt cctgg 25

<210> 413
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 413
 cggtagtgac tgtactctag tectgtttta caccocgtgg tgccg 45

<210> 414
 <211> 1196
 <212> DNA
 <213> Homo sapiens

<400> 414

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ggctcggcgc gggggtctt cctctttggc cagcccgact tctcctacaa 150
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gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

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His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln	20	25	30
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 cctggctcgc tgctgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
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<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<400> 419
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 ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100
 cgctgggtgt tctgtctcgc gatcagcctg ctcaactgct ccaacgccac 150
 gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
 tctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250
 tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300
 ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350
 tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgcccct gccagagcc tggcatctt 450
ctctccagcc aagctggctg ccttgtggtt cccagagcac cagcagacca 500
cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550
aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600
gctcgggtgc tataccatcc ctgtggcgt cgtctgctg ctgtccacca 650
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<210> 420
<211> 560
<212> PRT
<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg
1				5					10					15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val
				110					115					120
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu
				125					130					135
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu
				140					145					150
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met
				155					160					165
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val
				170					175					180
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met
				185					190					195
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser
				200					205					210
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala
				215					220					225
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys
				230					235					240
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys
				245					250					255

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
260	265		270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly
275	280		285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu
290	295		300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala
305	310		315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe
320	325		330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala
335	340		345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val
350	355		360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly
365	370		375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile
380	385		390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu
395	400		405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp	Trp
410	415		420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe	Ser
425	430		435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu	Gln
440	445		450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly	Gly
455	460		465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg	Ala
470	475		480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala	Arg
485	490		495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His	Pro
500	505		510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala	Thr
515	520		525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln	Ala
530	535		540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
560

<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag cctccttgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cggtcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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tggccttgcc ttgggggtcct gcttgtttca taatcatcta actatgggac 200

aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300

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 aaaaaaaaaa aaa 4313

<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly
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Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305		310 315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn
320		325 330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val
335		340 345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro
350		355 360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu
365		370 375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His
380		385 390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr
395		400 405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg
410		415 420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln
425		430 435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile
440		445 450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr
455		460 465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile
470		475 480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val
485		490 495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala Ile
500		505 510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr
515		520 525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser
530		535 540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu
545		550 555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu
560		565 570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr
575		580 585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	590	595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	605	610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	620	625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	635	640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn Val	650	655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile	665	670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	680	685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp Ser	695	700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val Ile	710	715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	725	730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	740	745	750
Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	755	760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro Val	770	775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg Thr	815	820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln Pro	860	865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 427

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<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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ggcctcgggg agtgggaagt ggaggagga ggcctcctta cacttcgcca 150

tgagtttccct catcgactcc agcatcatga ttacctccca gatactatct 200

tttggatttg ggtggctttt ctccatgcgc caattgttta aagactatga 250

gatacgtcag tatgtgttac aggtgatctt ctccgtgacg tttgcatttt 300

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 ttgacctga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
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 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 430

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			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser
			125						130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
			140						145					150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
			155						160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
			170						175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
	425	430	435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
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Lys Gln Met Ala	Pro		
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<210> 431

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

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ttgtaconggt gatctttctcc gtgacgtttg ccatttcttg caccatgttt 200
gagctcatca tctttgaaat cttnggagta ttgaatagca gctcccgta 250
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttntca 300
tggtgccctt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200
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tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aaatggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tgttgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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gggcctccgg gatctgtac ctttttggt cctgtcgt cgaactgctc 100

ttctcacggg ctgtgcctt caatctggac gtgatgggtg cttgacgcaa 150

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 a 3951

<210> 437
 <211> 1141
 <212> PRT
 <213> Homo sapiens

<400> 437
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 Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu
 35 40 45
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
 50 55 60
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
 65 70 75
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly
 80 85 90
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
 95 100 105

Val Asp Ile Asp Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile	Gly
	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln	Pro
	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val	Met
	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp	Pro
	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His	Val
	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val	Thr
	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr	Thr
	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln	Glu
	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu	Pro
	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe	Ser
	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp	Val
	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly	Gln
	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp	Pro
	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln	Val
	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys	Ser
	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp	Arg
	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly	Glu
	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala	Glu
	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala	Asn
	950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcagggagct gagtggacgg ctcgagacgg cggcgcggtgc 50

agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtggctta tcccagccct gtttgtgggt cagatggtca 600

tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgtaagaga gcatgcagtg acctggagtt 750

caggggaagtg gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

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 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20				25						30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys	35	40	45
	50	55	60
Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro	65	70	75
Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys	80	85	90
Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp	95	100	105
Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg	110	115	120
Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile	125	130	135
Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val	140	145	150
Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu	155	160	165
Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu	170	175	180
Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg	185	190	195
Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala	200	205	210
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser	215	220	225
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg	230	235	240
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp	245	250	255
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln	260	265	270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr	275	280	285
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile	290	295	300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro	305	310	315
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val			

	320		325		330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly					
	335		340		345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp					
	350		355		360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn					
	365		370		375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe					
	380		385		390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu					
	395		400		405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu					
	410		415		420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr					
	425		430		435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttaactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gagcggagac aacagtacct gacgcctctt tcagcccggg atgccccag 100
cagggatggg cgacaagatc tggtgcctt tccccgtgt ccttctggcc 150
gctctgcctc cgggtctgt gctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta ccttcccg cggccagaag gagtgcctt 250
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ctatggttaa tttagtggc atggtggtgg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850
tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950
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attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050
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cccagaactt ttttgtaaat gcggcagtta caaattaact gtggaagttt 1200
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taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150
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tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250
tcaagtacta gtaatttaac ttcacatga atgaactata atttttaagt 2300
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 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
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 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

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<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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gccctgccca gtgtgtctctg gatgctgctt tcttgctca ttctcctgtg 150
tcagggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
gctgtcccaa aggtccaag gcctatggct cccctgcta tgcttggtt 250
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
ctctggaaaa ctggtgtctg tgctcagtgg ggctgagga tcttcgtgt 350
cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
ccatcttaaa cctggccac tgtgggagcc tgtcaagaag cacaggattt 550
ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600
gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650
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gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850
aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
			20						25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
			35						40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
			50						55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
			65						70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
			80						85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
			95						100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
			110						115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
			125						130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
			140						145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
			155						160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
			170						175						

<210> 453
<211> 550
<212> DNA
<213> Homo sapiens

<400> 453

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ggcgctcctg gcgctgggtgc tggctgcctg cggagagctg gcgccggccc 150
tgcgctgcta cgtctgtccg gagccacacg gactgtcgga ctgtgtcacc 200
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
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gtgccagcaa gtgtaagccc tgggatgtgg atggcatcgg ccagaccctg 350
 ccctgtgctct gtgcaatac tgagctgtgc aatgtagacg gggcgcccg 400
 tctgaacagc ctccactgcg gggccctcac gctctcccca ctcttgagcc 450
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<210> 454
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 454
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 Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
 20 25 30
 Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
 35 40 45
 Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
 50 55 60
 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
 65 70 75
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
 80 85 90
 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
 95 100 105
 Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
 110 115 120
 Leu Ser Leu Arg Leu
 125

<210> 455
 <211> 1518
 <212> DNA
 <213> Homo sapiens

<400> 455
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 gcgcagcggg agctaccggg gtctttgtcg cgatggttagc ggcggctctc 200

ggaggccacc ctctgctggg agtgagcgcc acottgaact cggttctcaa 250
 ttccaaacgt atcaagaacc tgcccccacc gctggggggc gctgcggggc 300
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 aataagtacc agaccattga caactaccag ccgtaccogt gcgcagagga 400
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 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
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 ccttcaccaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
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 tttcagctta tagttcttaa aagcataacc ctttaccoca ttttaattcta 1350
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 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
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 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT
<213> Homo sapiens

<400> 456

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala	
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser	
				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
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<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
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cggcgccac cttntgctgg gagtgcgc caccttgaat cggttttcaa 250
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atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

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gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200
gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250
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accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400
agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450
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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe
650 655 660

Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val
665 670 675

Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln
680 685 690

Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr
695 700 705

Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg
710 715 720

Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr
725 730 735

Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu
740 745

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

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<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

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<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

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<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

<400> 463

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<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met	Asn	Ile	Ile	Leu	Glu	Ile	Leu	Leu	Leu	Leu	Ile	Thr	Ile	Ile	1	5	10	15
Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg	20	25	30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly				

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro		
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe		
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly		
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe		
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp		
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys		
290	295	300

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465
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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
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Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
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Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
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Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser		65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln		80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp		95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln		110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser		125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro		140	145	150
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Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg		170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro		185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala		200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys		215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys		230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe		245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe		260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro		275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe		290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu		305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His		320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu		335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg
				350					355					360
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser
				365					370					375
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln
				380					385					390
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr
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<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468
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 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
 50 55 60
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
 65 70 75
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
 80 85 90
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
 95 100 105
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
 110 115 120
 Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
 125 130 135
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
 140 145 150
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
 155 160 165
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
 170 175 180
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
 185 190 195
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Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
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 <211> 687
 <212> DNA
 <213> Homo sapiens

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 <211> 180
 <212> PRT
 <213> Homo sapiens

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Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu			
				50					55					60			
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn			
				65					70					75			
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu			
				80					85					90			
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile			
				95					100					105			
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg			
				110					115					120			
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp			
				125					130					135			
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg			
				140					145					150			
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln			
				155					160					165			
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 <211> 2368
 <212> DNA
 <213> Homo sapiens

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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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			20					25					30	
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
			35					40					45	
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
			50					55					60	
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
			65					70					75	
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
			80					85					90	
Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
			95					100					105	
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
			110					115					120	
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
			125					130					135	
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
			140					145					150	
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
			155					160					165	

Ile Ser Gly Lys	Ile Trp His Leu His Asn Tyr Phe Thr Val Thr	170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala	185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr	320	325	330
Glu Val Val Glu	Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala	335	340	345
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<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

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<210> 474

<211> 24

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<223> Synthetic oligonucleotide probe

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<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

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<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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 <212> PRT
 <213> Homo sapiens

<400> 477
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 Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val
 20 25 30
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
 170 175 180
 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195
 Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27
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<220>
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<400> 478
gtccacagac agtcacotca ggagcag 27

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acaagtgtct tcccaacctg 20

<210> 480
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<220>
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atcctcccag agccatggta cctc 24

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ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50
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<212> DNA
<213> Homo sapiens

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ccgtcggaggg aaaatgactc cccagtcgct gctgcagacg acaactgttcc 250
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<210> 483
 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483
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 20 25 30
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
 80 85 90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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gggactccct ggtcagctac atcaccaacc tgggctctt cagcctgggtg 500
ttctgttca acatgg 516

<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

ggcattggag cagtgcctggg tg 22

<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<400> 486

tgaggacctg gatggggctg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactacct 150
gogattctct gctgccagag caggctcggc gcttccacc cagtgcagcc 200
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gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
gaagtattca cagcccaagg ttctctcata ctatccaag aaatacggtc 500
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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe
				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

ccaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gggctatcc tctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	20	25	30	
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr	Lys Leu Lys Val Leu Ser
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Leu Lys Asp Asn Asn Val Thr Ala Val	Pro Thr Val Leu Pro Ser
215	220 225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn	Asn Met Ile Ala Lys Ile
230	235 240
Gln Glu Asp Asp Phe Asn Asn Leu Asn	Gln Leu Gln Ile Leu Asp
245	250 255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr	Asn Ala Pro Phe Pro Cys
260	265 270
Ala Pro Cys Lys Asn Asn Ser Pro Leu	Gln Ile Pro Val Asn Ala
275	280 285
Phe Asp Ala Leu Thr Glu Leu Lys Val	Leu Arg Leu His Ser Asn
290	295 300
Ser Leu Gln His Val Pro Pro Arg Trp	Phe Lys Asn Ile Asn Lys
305	310 315
Leu Gln Glu Leu Asp Leu Ser Gln Asn	Phe Leu Ala Lys Glu Ile
320	325 330
Gly Asp Ala Lys Phe Leu His Phe Leu	Pro Ser Leu Ile Gln Leu
335	340 345
Asp Leu Ser Phe Asn Phe Glu Leu Gln	Val Tyr Arg Ala Ser Met
350	355 360
Asn Leu Ser Gln Ala Phe Ser Ser Leu	Lys Ser Leu Lys Ile Leu
365	370 375
Arg Ile Arg Gly Tyr Val Phe Lys Glu	Leu Lys Ser Phe Asn Leu
380	385 390
Ser Pro Leu His Asn Leu Gln Asn Leu	Glu Val Leu Asp Leu Gly
395	400 405
Thr Asn Phe Ile Lys Ile Ala Asn Leu	Ser Met Phe Lys Gln Phe
410	415 420
Lys Arg Leu Lys Val Ile Asp Leu Ser	Val Asn Lys Ile Ser Pro
425	430 435
Ser Gly Asp Ser Ser Glu Val Gly Phe	Cys Ser Asn Ala Arg Thr
440	445 450
Ser Val Glu Ser Tyr Glu Pro Gln Val	Leu Glu Gln Leu His Tyr
455	460 465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser	Cys Arg Phe Lys Asn Lys
470	475 480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

<210> 497
<211> 4199
<212> DNA
<213> Homo sapiens

<400> 497
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His	440	445	450
Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser	455	460	465
Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala	470	475	480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu	515	520	525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser	755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	615	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
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<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
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Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
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Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
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Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu

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Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
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	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
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Lys Asp Ser					

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<211> 1700

<212> DNA

<213> Homo sapiens

<400> 507

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<211> 273

<212> PFT

<213> Homo sapiens

<400> 508

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg	50	55	60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg	65	70	75
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro	80	85	90
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala	95	100	105
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro	110	115	120
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln	125	130	135
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln	140	145	150
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu	155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly	170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala	185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu	200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala	215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu	230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu	245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys	260	265	270

Lys Asp Ser

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
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Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
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Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
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<213> Homo sapiens

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 gggatcctaa ctgggttctt ggggtcttca ggactgaaga ggaggagag 1950
 tggggtcaga agattctctt ggcacccaag tgcagcatt gccacaaaa 2000
 ccttttagga atgggacagg taccttccac ttgtgtann nnnnnnnnn 2050
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 attatatgtg gctatatttc ctagagcacc tgtgttttcc tctttctaag 2600
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 tttcatcta ttgaaggcg attaaactgt gtctaataca 2690

<110> 515

<111> 364

<112> PRT

<113> Homo sapiens

<400> 515

Met	Ser	Val	Met	Val	Val	Arg	Lys	Lys	Val	Thr	Arg	Lys	Trp	Glu
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu			
	320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu			
	335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala			
	350	355	360
Glu Ala Glu Lys			

<210> 516

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 38, 88, 118, 135, 193, 213, 222

<223> unknown base

<400> 516

aaaaccctgt attttttaca atgcaaata gacaatnanc tggaggtctt 50

tgaattaggt attataggga tgggtggggtt gatttttntt cctggagggt 100

tttggttttg gactctcnc tttcccaca gagcnccttg accatcactg 150

ccccgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200

tcttcactct tntctctcc cncctcaca totatgtctt cgccttcaac 250

atcgt 255

<210> 517

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

aaacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaacc attttgggag caggaattcc aatcatgtct gtgatgggtg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaaa atcatgaaaa ccattccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg ccogtgcgca ggggagatgc caccctcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagaggg ccaccctcag 300

gtgcactatt gacaaccggg tcaccggggt ggccctggcta aaccgcagca 350

ccatcctcta tgttgggaat gacaagtggg gcctggatcc tcgcgtgggc 400

ottctgagca acacccaaac gcagtagcgc atcgagatcc agaacgtgga 450
 tgtgtatgac gagggccctt acactgctc ggtgcagaca gacaaccacc 500
 caaagacctc tagggccac ctcattgtgc aagtatctcc caaaattgta 550
 gagattttct cagatatctc cattaatgaa gggaacaata ttagcctcac 600
 ctgcatagca actggtagac cagagcctac ggtaacttgg agacacatct 650
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 ggcacacccc gggagcagtc aggggactac gagtgcagtg cctccaatga 750
 cgtggccgcg cccgtggtac ggagagtaaa ggtcacccgtg aactatccac 800
 catacatttc agaagccaag ggtacaggtg tcccctgtgg abaaaagggg 850
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 cagcatcatg ctatttggtc caggcccgct cagcgaggtg agcaacggca 1100
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 gcgcccacca ccaccacca cacaacagca atggcaaac ccacagcaac 1250
 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300
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 aaaaagaaat tgaatttgc cttgcagata tttaggtaca atggagtttt 1400
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 aattcaatca gtccatagag acgaacagaa tgajaccttc cggcccaagc 1600
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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

Met	Lys	Thr	Ile	Gln	Pro	Lys	Met	His	Asn	Ser	Ile	Ser	Trp	Ala
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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro
			20						25					30
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val
			35						40					45
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp
			50						55					60
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu
			65						70					75
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu
			80						85					90
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val
			95						100					105
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp
			110						115					120
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser
			125						130					135
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly
			140						145					150
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro
			155						160					165
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val
			170						175					180
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln
			185						190					195
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro
			200						205					210
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile
			215						220					225
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr
			230						235					240
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp
			245						250					255
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys
			260						265					270
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val
			275						280					285

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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tcgggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200
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acctgctcgg tgcagacaga caaccacca aagacctcta gggccacct 400
cattgtgcaa gtatctccca aaattgtaga gatttcttca gatctctcca 450
ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500
gag 503

<210> 525

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

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tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
aaggggacaa gacagctgtt aggcacagc aggcagctgg agctgggtctt 200
agcaggtgcc ttctacttgc tggctgcaat gcttctgggc tgcttctgtg 250

ccctaggggt ccagtaccac agagacccat cccacagcac ctgccttaca 300
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ctctgggacc aaaaccaggc catactgaag cactgtctg aaaacaccac 500
cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550
cttgccctaca ggtggagcgc attgaggagc tgggagccca gccactgaga 600
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acatggagga actggggatg ctgctgggtg ggcggccac ctccacgagg 900
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 cctccagcag agccccacc attcactgtg acatctttcc gtgtcaccct 2550
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 cc 2602

<210> 526

<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

Met	Asn	Val	Ala	Leu	Gln	Glu	Leu	Gly	Ala	Gly	Ser	Asn	Val	Gly
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				20				25					30	
Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu
				35				40					45	
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro
				50				55					60	

Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly	65	70	75
Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp	80	85	90
Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu	95	100	105
Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp	110	115	120
Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe	125	130	135
Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu	140	145	150
Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro	155	160	165
Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly	170	175	180
Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala	185	190	195
Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala	200	205	210
Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser	215	220	225
Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala	230	235	240
Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu	245	250	255
Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met	260	265	270
Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val	275	280	285
Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met	290	295	300
Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu	305	310	315
Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser	320	325	330
Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser	335	340	345

Glu	Leu	Ile	Asn	Arg	Thr	Glu	Pro	Ser	Ile	Leu	Asn	Asn	Tyr	Leu	350	355	360
Ile	Trp	Asn	Leu	Val	Gln	Lys	Thr	Thr	Ser	Ser	Leu	Asp	Arg	Arg	365	370	375
Phe	Glu	Ser	Ala	Gln	Glu	Lys	Leu	Leu	Glu	Thr	Leu	Tyr	Gly	Thr	380	385	390
Lys	Lys	Ser	Cys	Val	Pro	Arg	Trp	Gln	Thr	Cys	Ile	Ser	Asn	Thr	395	400	405
Asp	Asp	Ala	Leu	Gly	Phe	Ala	Leu	Gly	Ser	Leu	Phe	Val	Lys	Ala	410	415	420
Thr	Phe	Asp	Arg	Gln	Ser	Lys	Glu	Ile	Ala	Glu	Gly	Met	Ile	Ser	425	430	435
Glu	Ile	Arg	Thr	Ala	Phe	Glu	Glu	Ala	Leu	Gly	Gln	Leu	Val	Trp	440	445	450
Met	Asp	Glu	Lys	Thr	Arg	Gln	Ala	Ala	Lys	Glu	Lys	Ala	Asp	Ala	455	460	465
Ile	Tyr	Asp	Met	Ile	Gly	Phe	Pro	Asp	Phe	Ile	Leu	Glu	Pro	Lys	470	475	480
Glu	Leu	Asp	Asp	Val	Tyr	Asp	Gly	Tyr	Glu	Ile	Ser	Glu	Asp	Ser	485	490	495
Phe	Phe	Gln	Asn	Met	Leu	Asn	Leu	Tyr	Asn	Phe	Ser	Ala	Lys	Val	500	505	510
Met	Ala	Asp	Gln	Leu	Arg	Lys	Pro	Pro	Ser	Arg	Asp	Gln	Trp	Ser	515	520	525
Met	Thr	Pro	Gln	Thr	Val	Asn	Ala	Tyr	Tyr	Leu	Pro	Thr	Lys	Asn	530	535	540
Glu	Ile	Val	Phe	Pro	Ala	Gly	Ile	Leu	Gln	Ala	Pro	Phe	Tyr	Ala	545	550	555
Arg	Asn	His	Pro	Lys	Ala	Leu	Asn	Phe	Gly	Gly	Ile	Gly	Val	Val	560	565	570
Met	Gly	His	Glu	Leu	Thr	His	Ala	Phe	Asp	Asp	Gln	Gly	Arg	Glu	575	580	585
Tyr	Asp	Lys	Glu	Gly	Asn	Leu	Arg	Pro	Trp	Trp	Gln	Asn	Glu	Ser	590	595	600
Leu	Ala	Ala	Phe	Arg	Asn	His	Thr	Ala	Cys	Met	Glu	Glu	Gln	Tyr	605	610	615
Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr	620	625	630

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr		
	635	645
Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln		
	650	660
Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly		
	665	675
Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His		
	680	690
Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val		
	695	705
Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly		
	710	720
Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val		
	725	735

Trp

<210> 527
 <211> 4308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1478, 3978, 4057-4058, 4070
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<400> 527
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<400> 599

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gactacaagg cgctcagcta 20

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 611
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<212> DNA
<213> Homo Sapien

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accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200
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<210> 612

<211> 352

<212> PRT

<213> Homo Sapien

<400> 612

Met	Met	Leu	Leu	Val	Gln	Gly	Ala	Cys	Cys	Ser	Asn	Gln	Trp	Leu
1				5						10				15

Ala	Ala	Val	Leu	Leu	Ser	Leu	Cys	Cys	Leu	Leu	Pro	Ser	Cys	Leu
				20					25					30

Pro	Ala	Gly	Gln	Ser	Val	Asp	Phe	Pro	Trp	Ala	Ala	Val	Asp	Asn
				35					40					45

Met	Met	Val	Arg	Lys	Gly	Asp	Thr	Ala	Val	Leu	Arg	Cys	Tyr	Leu
				50					55					60

Glu	Asp	Gly	Ala	Ser	Lys	Gly	Ala	Trp	Leu	Asn	Arg	Ser	Ser	Ile
				65					70					75

Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
				80					85					90

Ile	Ser	Thr	Leu	Asn	Lys	Arg	Asp	Tyr	Ser	Leu	Gln	Ile	Gln	Asn
				95					100					105

Val	Asp	Val	Thr	Asp	Asp	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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aaataagaaa attctcaagg aggacgagct cttgagttag acccaacaag 150
ctgcttttca ccaaattgca atggagcctt togaaatcaa tgttccaaag 200
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tggagaacac ctggctcagg gtgcactgag gctgcaagtc ctgcaggccc 450
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gcccgcggg accactgct gagaaggag ccaagggggt tatgggacga 650
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ctggcaccac aggaaccaca ggagagaagg gcagcaaagg cgatgggggt 800
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 gcgtctgacc cggaaccctt ttcacttctc tgcctccgag gtgtcctcgg 1700
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<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

Met	Arg	Asn	Lys	Lys	Ile	Leu	Lys	Glu	Asp	Glu	Leu	Leu	Ser	Glu	1	5	10	15
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Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				

185	190	195
Gly Pro Pro Gly Val Lys Gly Glu Ala	Gly Leu Gln Gly Pro Gln	
200	205	210
Gly Ala Pro Gly Lys Gln Gly Ala Thr	Gly Thr Pro Gly Pro Gln	
215	220	225
Gly Glu Lys Gly Ser Lys Gly Asp Gly	Gly Leu Ile Gly Pro Lys	
230	235	240
Gly Glu Thr Gly Thr Lys Gly Glu Lys	Gly Asp Leu Gly Leu Pro	
245	250	255
Gly Ser Lys Gly Asp Arg Gly Met Lys	Gly Asp Ala Gly Val Met	
260	265	270
Gly Pro Pro Gly Ala Gln Gly Ser Lys	Gly Asp Phe Gly Arg Pro	
275	280	285
Gly Pro Pro Gly Leu Ala Gly Phe Pro	Gly Ala Lys Gly Asp Gln	
290	295	300
Gly Gln Pro Gly Leu Gln Gly Val Pro	Gly Pro Pro Gly Ala Val	
305	310	315
Gly His Pro Gly Ala Lys Gly Glu Pro	Gly Ser Ala Gly Ser Pro	
320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	

470

475

480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu
 485 490 495

Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His
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Glu Glu Asp Ala Gly Val Glu Cys Ser Val
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<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaa 647

<210> 616

<211> 98

<212> PRT

<213> Homo Sapien

<400> 616

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Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
50 55 60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
65 70 75

Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
80 85 90

Phe Val Ile Pro Cys Asn Asn Gln
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<210> 617

<211> 2558

<212> DNA

<213> Homo Sapien

<400> 617

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Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val
215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys
230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg
245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro
260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu
275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr
290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro
305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly
320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His
335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly
350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly
365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser
380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu
395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser
410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala
425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile
440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp
455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu
470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu
485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn Asp	Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

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<210> 623

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<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide probe

<400> 624

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